The dissimilation of sulfur compounds is likely to have been one of the earliest energy metabolism in the early Earth. However, many questions remain about how energy is conserved in sulfur-metabolizing organisms. A key reaction in microbial sulfur metabolism is the reduction of sulfite by the siroheme-containing dissimilatory sulfite reductase, DsrAB. This enzyme is present in sulfate, thiosulfate and sulfite reducing organisms, and also in sulfur-oxidizers where it is thought to operate in reverse. The mechanism of sulfite reduction by DsrAB has long been the subject of controversy due to the *in vitro* formation of thiosulfate and trithionate, in contrast to the closely-related assimilatory enzyme that produces only sulfide.

Recent studies have identified the small protein DsrC [1] and the DsrMKJOP membrane complex as physiological partners of DsrAB [2]. In particular, a crystal structure of DsrAB in complex with DsrC suggested the direct involvement of the latter protein in sulfite reduction and led to the proposal of a new mechanism for this reaction [3]. I will present recent *in vivo* and *in vitro* studies that reveal the function of DsrC in sulfite reduction, identifying the mechanism and physiological product of this reaction. These results implicate the respiratory membrane complex DsrMKJOP in the process, providing a direct link to energy conservation.

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S8.L4

A genomic view on syntrophic versus non-syntrophic lifestyle of anaerobic fatty acid-degrading bacteria

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In sulfate-reducing and methanogenic environments complex biopolymers are degraded by fermentative micro-organisms that produce hydrogen, carbon dioxide and short chain fatty acids. Degradation of short chain fatty acids can be coupled to methanogenesis or to sulfate reduction. We applied a genomic approach to understand why some bacteria are able to grow in syntrophy with methanogens and others are not. Bacterial strains were selected based on genome availability and upon their ability to grow on short chain fatty acids alone or in syntrophic association with methanogens. Systematic functional domain profiling allowed us to shed light on this fundamental and ecologically important question. Extra-cytoplasmic formate dehydrogenases, including their maturation protein are a typical difference between syntrophic and non-syntrophic butyrate and propionate degraders. Furthermore, two domains with a currently unknown function seem to be associated with the ability of syntrophic growth. One is putatively involved in capsule or biofilm production and a second in cell division, shape-determination or sporulation. Some sulfate reducing bacteria have never been tested for syntrophic growth, but as all crucial domains were found in their genomes, it is possible that these are able to grow in syntrophic association with methanogens. In addition, profiling domains involved in electron transfer mechanisms revealed the important role of the Rnf-complex and the formate transporter in syntrophy, and indicates that DUF224 may have a role in electron transfer in bacteria that show syntrophic growth.

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S8.O1

Spatio-temporal organization of a prokaryotic respiratory complex

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Oxidative phosphorylation (OXPHOS) is an essential process, for most living organisms, sustained by multisubunit complexes anchored in the lipid bilayer. The basic principle of OXPHOS applies to the respiratory electron transfer chains of eukaryotes and prokaryotes. Plasticity is a hallmark of the OXPHOS process. In eukaryotes, mitochondria are dynamic compartments fine-tuning their activity in response to changes in nutrient availability and oxygen concentrations through a plastic organization of the OXPHOS complexes in the membrane. Such a plastic organization consists in a balanced distribution between isolated complexes and supercomplexes [1]. Similarly, prokaryotes are characterized by the coexistence of several complexes both at the electron input and output leading to multiple electron transfer routes. Such a metabolic flexibility accounts for colonization of multiple environments and adaptation to environmental changes [2]. An immediate question concerns the cellular organization of OXPHOS in living organisms i.e. how are the complexes distributed across the membrane? Is there a dynamic distribution? Furthermore, does such organization have functional implications? Through the use of fluorescent protein tagging, we have characterized at a single-cell level the distribution of the nitrate reductase from *Escherichia coli*, an anaerobic OXPHOS complex largely represented in prokaryotes. Apart from observing a submicrometric localization of the complex at the bacterial cell poles, its distribution within the cytoplasmic membrane is strongly influenced by environmental signals, that is, in response to the metabolic demand. We provide here the identification of an unprecedented polar cue and describe the functional implications of such spatio-temporal regulation and associated mechanism.

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